

ATG ACC GAT CCA CGT CAG CTG CAC CTG GCC CAG TTC TTC TGT GCC GGC AAC GTC ACG CAC	50
M T D P R Q L H L A G F C A G N V T H>	
GCC CAC GGA GCG TGG CGC CAC GCC GAC GAC TCC AAC GGC TTC CTC ACC AAG GAG TAC TAC	120
A H G A W R H A D D S N G F L T K E Y Y>	
CAG CAG ATT GCC CGC ACG CTC GAG CGC GGC AAG TTC GAC CTG CTG L L F L P D A>	180
Q Q I A R T L E R G K F D L L F L P D A>	
CTC GCC GTG TGG GAC AGC TAC GGC GAC AAT CTG GAG ACC GGT CTG CGG TAT EGC GGG CAA	240
L A V W D S Y G D N L E T G L R Y G G Q>	
GGC GCG GTG ATG CTG GAG CCC GGC GTA GTT ATC GCC GCG ATG GCC TCG GTG ACC GAA CAT	300
G A V M L B P G V I A A M A S V T E H>	
CTG GGG CTG GGC GCC ACC ATT TCC ACC ACC TAC TAC CCG CCC TAC CAT GTA GCC CGG GTC	360
L G L G A T I S S T T Y Y P P Y H V A R V>	
GTC GCT TCG CTG GAC CAG CTG TCC TCC GGC CGA GTG TCG TGG AAC GTG ACC TCG CTC	420
V A S L D Q L S S S G R V S W N V T S L>	

FIGURE 1A

FIGURE 1B

Sphingomonas ORF1 (cont.)

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      870      *
GCG GTG ATG CCG ATC CTC GGC GAG ACC GAG GCG ATC GCC AGG CAG CGT CTC GAA TAC ATA
A V M P I L G E T E A I A R Q R L E Y I>
      960
AAT TCG CTG GTG CAT CCC GAA GTC GGG CTT TCT ACG TTG TCC AGC CAT GTC GGG GTC AAC
N S L V H P E V G L S T L S S H V G V N>
      990
CTT GCC GAC TAT TCG CTC CTC GAT ACC CCG CTG ACC GAG GTC CTG GGC GAT CTC GCC CAG CGC
L A D Y S L D T P L T E V L G D L A Q R>
      1050
AAC GTG CCC ACC CAA CTG GGC ATG TTC GCC AGG ATG TTG CAG GCC GAG ACG CTG ACC GTG
N V P T Q L G M F A R M L Q A E T L T V>
      1110
GGA GAA ATG GGC CCG CGT TAT GGC GCC AAC GTG GGC TTC GTC CCG CAG TGG GCG GGA ACC
G E M G R R Y G A N V G F V P Q W A G T>
      1170
CGC GAG CAG ATC GCG GAC CTG ATC GAG ATC CAT TTC AAG GCC GGC GGC GAT GGC TTC
R E Q I A D L I E I H P K A G G A D G F>
      1230
ATC ATC TCG CCG GCG TTC CTG CCC GGA TCT TAC GAG GAA TTC GTC GAT CAG GTG GTG CCC
I I S P A F L P G S Y E E F V D Q V V P>

```

FIGURE 1C

Country	Year	Value	Unit
Algeria	1980	1.00	1000
Algeria	1981	1.00	1000
Algeria	1982	1.00	1000
Algeria	1983	1.00	1000
Algeria	1984	1.00	1000
Algeria	1985	1.00	1000
Algeria	1986	1.00	1000
Algeria	1987	1.00	1000
Algeria	1988	1.00	1000
Algeria	1989	1.00	1000
Algeria	1990	1.00	1000
Algeria	1991	1.00	1000
Algeria	1992	1.00	1000
Algeria	1993	1.00	1000
Algeria	1994	1.00	1000
Algeria	1995	1.00	1000
Algeria	1996	1.00	1000
Algeria	1997	1.00	1000
Algeria	1998	1.00	1000
Algeria	1999	1.00	1000
Algeria	2000	1.00	1000
Algeria	2001	1.00	1000
Algeria	2002	1.00	1000
Algeria	2003	1.00	1000
Algeria	2004	1.00	1000
Algeria	2005	1.00	1000
Algeria	2006	1.00	1000
Algeria	2007	1.00	1000
Algeria	2008	1.00	1000
Algeria	2009	1.00	1000
Algeria	2010	1.00	1000
Algeria	2011	1.00	1000
Algeria	2012	1.00	1000
Algeria	2013	1.00	1000
Algeria	2014	1.00	1000
Algeria	2015	1.00	1000
Algeria	2016	1.00	1000
Algeria	2017	1.00	1000
Algeria	2018	1.00	1000
Algeria	2019	1.00	1000
Algeria	2020	1.00	1000
Algeria	2021	1.00	1000
Algeria	2022	1.00	1000
Algeria	2023	1.00	1000
Algeria	2024	1.00	1000
Algeria	2025	1.00	1000
Algeria	2026	1.00	1000
Algeria	2027	1.00	1000
Algeria	2028	1.00	1000
Algeria	2029	1.00	1000
Algeria	2030	1.00	1000
Algeria	2031	1.00	1000
Algeria	2032	1.00	1000
Algeria	2033	1.00	1000
Algeria	2034	1.00	1000
Algeria	2035	1.00	1000
Algeria	2036	1.00	1000
Algeria	2037	1.00	1000
Algeria	2038	1.00	1000
Algeria	2039	1.00	1000
Algeria	2040	1.00	1000
Algeria	2041	1.00	1000
Algeria	2042	1.00	1000
Algeria	2043	1.00	1000
Algeria	2044	1.00	1000
Algeria	2045	1.00	1000
Algeria	2046	1.00	1000
Algeria	2047	1.00	1000
Algeria	2048	1.00	1000
Algeria	2049	1.00	1000
Algeria	2050	1.00	1000
Algeria	2051	1.00	1000
Algeria	2052	1.00	1000
Algeria	2053	1.00	1000
Algeria	2054	1.00	1000
Algeria	2055	1.00	1000
Algeria	2056	1.00	1000
Algeria	2057	1.00	1000
Algeria	2058	1.00	1000
Algeria	2059	1.00	1000
Algeria	2060	1.00	1000
Algeria	2061	1.00	1000
Algeria	2062	1.00	1000
Algeria	2063	1.00	1000
Algeria	2064	1.00	1000
Algeria	2065	1.00	1000
Algeria	2066	1.00	1000
Algeria	2067	1.00	1000

FIGURE 1D

Sphingomonas ORF2

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30      *
ATG ACG ACA GAC ATC CAC CCG GCG AGC GCC GCA TCG TCG CCG GCG CGC GCG ACG ATC
M T T D I H P A S A A S S S P A A R A T I>
60      *

90      *
ACC TAC AGC AAC TGC CCC GTG CCT AAT GCC CTG CTC GCC GCG CTC GGC TCA GGT ATT CTG
T Y S N C P V T L A L L A L A A L G S G I L>
120      *

150      *
GAC AGT GCC GGG ATC ACA CTT GCC CTG CTG ACC GGA AAG CAG GGC GAG GTG CAC TTC ACC
D S A G I T L A L L A L L T G K Q G E V H F T>
180      *

210      *
TAC GAC CGA GAT GAC TAC ACC CGC TTC GGC GGC GAG ATT CCG CCG CTG GTC AGC GAG GGA
Y D R D D Y T R F G G G E I P P L V S E G>
240      *

270      *
CTG CGT GCG CCG GGG CCG ACC CGC CTG CTG GGA CTG ACG CCG GTG CTG GGC CGC TGG GGC
L R A P G R T R L L G L T P V L G R W G>
300      *

330      *
TAC TTC GTC CCG GGC GAC AGC GCG ATC CCG ACC CCG GCC GAT CTT GCC GGC CGC CGC GTC
Y F V R G D S A I R T P A D L A G R R V>
360      *

390      *
GGA GTA TCC GAT TCG GCC AGG AGG ATA TTG ACC GGA AGG CTG GGC GAC TAC CGC GAA CTT
G V S D S A R R I L T G R L G D Y R E L>
420      *

```

FIGURE 2A

Sphingomonas ORF2 (cont)

450 * * * * *
 GAT OCC TGG CCG CAG ACC CTG GTC GCG CTG GCG ACA TGG GAG GCG CGT GCC TTG CTG AGC
 D P W R Q T L V A L G T W E A R A L L S>
 510 * * * * *
 ACG CTC GAG ACG GCG GGG CTT GGC GTC GGC GAC GTC GAG CTG ACG CGC ATC GAG AAC CCG
 T L E T A G L G V G D V E L T R I E N P>
 570 * * * * *
 TTC GTC GAC GTG CCG ACC GAA CGA CTG CAT GCC GGC TCG CTC AAA GGA ACC GAC CTG
 F V D V P T E R L H A A G S L K G T D L>
 630 * * * * *
 TTC CCC GAC GTG ACC AGC CAG CAG GCC GCA GTC CTT GAG GAT GAG CGC GCC GAC GCC CTG
 F P D V T S Q Q A A V L E D E R A D A L>
 690 * * * * *
 TTC CCG TGG CTT CCC TGG GCG GCC GAG CTC GAG ACC CCG ATC GGT GCA CGG CCG GTC CTA
 F A W L P P W A A E L E T R I G A R P V L>
 750 * * * * *
 GAC CTC AGC GCA GAC GAC CGC AAT GCC TAT GCG AGC ACC TGG ACG GTG AGC GCC GAG CTG
 D L S A D D R N A Y A S T W T V S A E L>
 810 * * * * *
 GTG GAC CCG CAG CCC GAA CTG GTG CAG CCG CTC GAT GAT GCG GTG GAT GCA GGG CCG
 V D R Q P E L V Q R L V D A V V D A G R>

FIGURE 2B

Sphingomonas ORF2 (cont.)

TGG GCC GAG GCC AAT GGC GAT GTC GTC TCC CGC CTG CAC GCC GAT AAC CTC GGT GTC AGT	970	*	*	*	980	*
W A E A N G D V V S S R L H A D N L G V S>						
CCC GAA AGC GTC CGC CAG GGA TTC GGA GCC GAT TTT CAC CGC CGC CTG ACG CCG CGG CTC	930	*	*	*	960	*
P E S V R Q G G F G A D F H R R L T P R L>						
GAC AGC GAT GCT ATC GCC ATC CTG GAG CGT ACT CAG CGG TTC CTG AAG GAT GCG AAC CTG	990	*	*	*	1020	*
D S D A I A I L E R T Q R F L K D A N L>						
ATC GAT CGG TCG TTG GCG CTC GAT CGG TGG GCT GCA CCT GAA TTC CTC GAA CAA AGT CTC	1050	*	*	*	1080	*
I D R S L A L D R W A A P E F L E Q S L>						
TCA CGC CAG GTC GAA GGG CAG ATA GCA TGA	1110	*	*	*		
S R Q V E G Q I A *>						

FIGURE 2C

Sphingomonas ORF3

10 * 20 * 30 * 40 * 50 * 60 *
 ATG AAC GAA CTC GTC AAA GAT CTC GGC CTC AAT CGA TCC GAT CCG ATC GGC GCT GTG CGG
 M N E L V K D L G L N R S D P I G A V R>

 70 * 80 * 90 * 100 * 110 * 120 *
 CGA CTG GCC GCG CAG TGG GGG GCC ACC GCT GTT GAT CGG GAC CGG GCC GGA TCG GCA
 R L A A Q W G A T A V D R D R A G S A>

 130 * 140 * 150 * 160 * 170 * 180 *
 ACC GCC GAA CTC GAT CAA CTG CGC GGC AGC GGC CTG CTC TCG CTG TCC ATT CCC GCC GCA
 T A E L D Q L R G S G L L S L S I P A A>

 190 * 200 * 210 * 220 * 230 * 240 *
 TAT GGC TGG GGC GCC GAC TGG CCA ACG ACT CTG GAA GTT ATC CGC GAA GTC GCA ACG
 Y G G W G A D W P T T L E V I R E V A T>

 250 * 260 * 270 * 280 * 290 * 300 *
 GTG GAC GGA TCG CTG GCG CAT CTA TTC GGC TAC CAC CTC GGC TGC GTA CCG ATG ATC GAG
 V D G S L A H L F G Y H L G C V P M I E>

 310 * 320 * 330 * 340 * 350 * 360 *
 CTG TTC GGC TCG GCG CCA CAA AAG GAA CCG CTG TAC CGC CAG ATC GCA AGC CAT GAT TGG
 L F G S A P Q K E R L Y R Q I A S H D W>

 370 * 380 * 390 * 400 * 410 * 420 *
 CGG GTC GGG AAT GCG TCG AGC GAA AAC AAC AGC CAC GTG CTC GAG TGG AAG CTT GCC GCC
 R V G N A S S E N N S H V L E W K L A A>

FIGURE 3A

Sphingomonas ORF3 (cont)

FIGURE 3B

Sphingomonas ORF3 (cont)

CCC GCC GGC GTG GCG AAG GCG ACA GAG GAT CCC CAC ATC ATC GCC ACC TAC GGT GAA CTG P A G V A K A T E D P H I I A T Y G E L>	850	860	870	880	890	900
	*	*	*	*	*	*
GCG ATC GCG CTC CAG GGC GCG GAG GCG GCC GCG GAG GTC GCG GCC CTG TTG CAA CAG A I A L Q G A E A A A R E V A A L L Q Q>	910	920	930	940	950	960
	*	*	*	*	*	*
GCG TGG GAC AAG GGC GAT GCG GTG ACG CCC GAA GAG CGC GGC GAG CTG ATG GTG AAG GTT A W D K G D A V T P E E R G Q L M V K V>	970	980	990	1000	1010	1020
	*	*	*	*	*	*
TCG GGT GTG AAG GCC CTC TCG ACG AAG GCC GCC CTC GAC ATC ACC AGC CGT ATT TTC GAG S G V K A A L S T K A A A L D I T S R I F E>	1030	1040	1050	1060	1070	1080
	*	*	*	*	*	*
ACA ACG GGC TCG CGA TCG ACG CAT CCC AGA TAC GGA TTC GAT CGG TTC TGG CGT AAC ATC T T G S R S T H P R Y G F D I V R N I>	1090	1100	1110	1120	1130	1140
	*	*	*	*	*	*
CAG ACT CAT ACG CTG CAC GAT CCG GTA TCG TAT AAA ATC GTC GAT GTG GGG AAC TAC ACG R T H T L H D P V S Y K I V D V G N Y T>	1150	1160	1170	1180	1190	1200
	*	*	*	*	*	*
CTC AAC GGG ACA TTC CCG GTT CCC GGA TTT ACG TCA L N G T F P V P G F T S>	1210	1220	1230			
	*	*	*			

FIGURE 3C

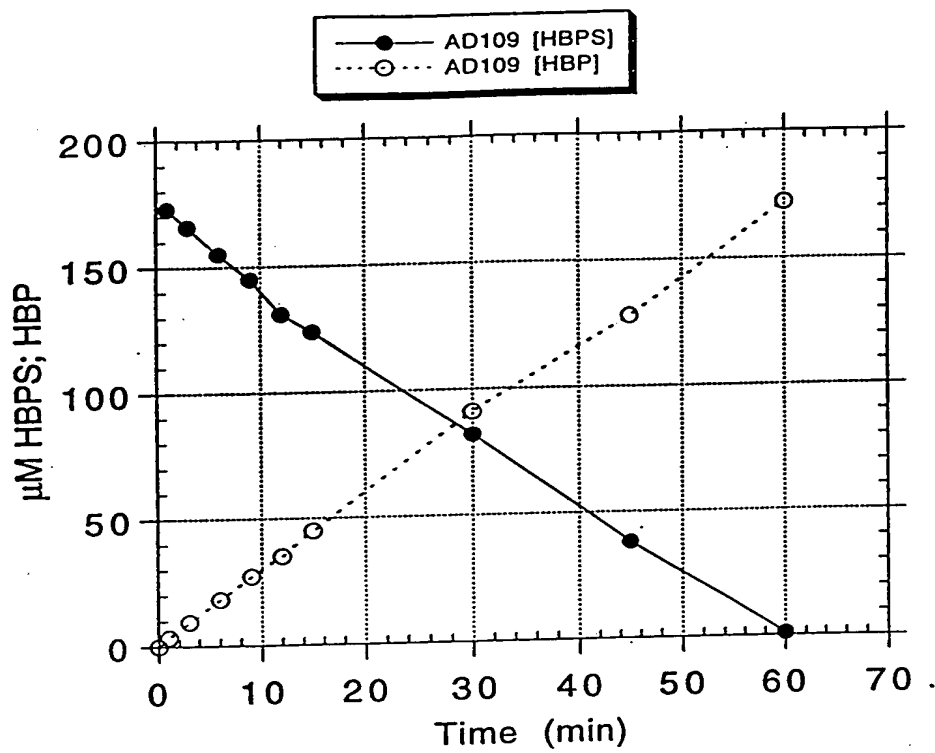


FIGURE 4

200 bp

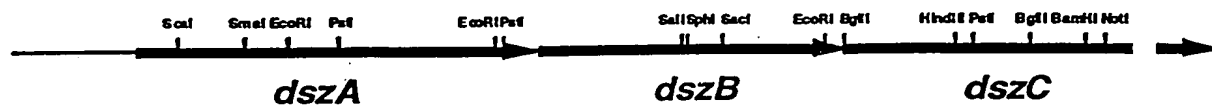


FIGURE 5

Sphingomonas dsz sequence

10	20	30	40	50	60
*	*	*	*	*	*
GGTTCGAGAT	CGATCTGACC	GTCGAACCCG	GCGCGGTTCA	AACCATCCTC	TGGGGCCTCT
CCAAGCTCTA	GCTAGACTGG	CAGCTTGGGC	CGCGCCAAGT	TTGGTAGGAG	ACCCCGGAGA
70	80	90	100	110	120
*	*	*	*	*	*
TCTTGCACTT	GACATAGGAA	TCTCTACTAA	ATAAATAGAT	ATTTATTCTGA	CACTAAGTTC
AGAACGTGAA	CTGTATCCTT	AGAGATGATT	TATTTATCTA	TAAATAAGCT	GTGATTCAAG
130	140	150	160	170	180
*	*	*	*	*	*
GGTGATCAGG	CCGACCGTGT	GTCTCAAGTG	CTCGCTCCGG	GTTGCCACGA	GCTAAAGCGC
CCACTAGTCC	GGCTGGCACA	CAGAGTTCAC	GAGCGAGGCC	CAACGGTGCT	CGATTTTCGG
190	200	210	220	230	240
*	*	*	*	*	*
GCGATGCTGG	GGCGACAGCG	CTAGGCATTG	CGTTCCCTCA	CACCAATGAT	GAGATGATAC
CGCTACGACC	CCGCTGTTCG	GATCCGTAAC	GCAAGGGAGT	GTGGTTACTA	CTCTACTATG
250	260	270	280	290	300
*	*	*	*	*	*
GATGCGCATG	ACCACTATCC	GCACCTAGCA	CGAAAGATCC	GTGCATTTTCG	CGAATGCCAA
CTACGCGTAC	TGGTGATAGG	CGTGATCGT	GCTTTCTAGG	CACGTAAAGC	GCTTACGGTT
310	320	330	340	350	360
*	*	*	*	*	*
TGAAGAGGAC	CGACGTACGG	CAGCTTCCTA	CGCTTTCGCG	CCATCGTTCA	TAGCCAAGGT
ACTTCTCCTG	GCTGCATGCC	GTCGAAGGAT	GCGAAAGCGC	GGTAGCAAGT	ATCGGTTCCA
370	380	390	400	410	420
*	*	*	*	*	*
CTTTTCGACG	CCGGTTTCGG	TGGGCGACTG	ACGGCGGTAG	CGCCGCGACT	ATTCGTTTCA
GAAAAGCTGC	GGCCAAGCGC	ACCCGCTGAC	TGCCGCCATC	GCGGCGCTGA	TAAGCAAAGT
430	440	450	460	470	480
*	*	*	*	*	*
AACTCACGAG	GATAAGAGCC	TATGACCGAT	CCACGTCAGC	TGCACCTGGC	CGGATTCTTC
TTGAGTGCTC	CTATTCTCGG	ATACTGGCTA	GGTGCAGTCG	ACGTGGACCG	GCCTAAGAAG
490	500	510	520	530	540
*	*	*	*	*	*
TGTGCCGGCA	ACGTCACGCA	CGCCACGGA	GCGTGGCGCC	ACGCCGACGA	CTCCAACGGC
ACACGGCCGT	TGCAGTGCCT	GCGGGTGCCT	CGCACC GCGG	TGCGGCTGCT	GAGGTTGCCG
550	560	570	580	590	600
*	*	*	*	*	*
TTCTCACCA	AGGAGTACTA	CCAGCAGATT	GCCCCGACGC	TCGAGCGCGG	CAAGTTCGAC
AAGGAGTGGT	TCCTCATGAT	GGTCGTCTAA	CGGGCGTGCG	AGCTCGCGCC	GTTCAAGCTG

FIGURE 6A

Sphingomonas dsz sequence (page 2)

610	620	630	640	650	660
*	*	*	*	*	*
CTGCTGTTCC	TTCCCCGACGC	GCTCGCCGTG	TGGGACAGCT	ACGGCGACAA	TCTGGAGACC
GACGACAAGG	AAGGGCTGCG	CGAGCGGCAC	ACCCTGTCTGA	TGCCGCTGTT	AGACCTCTGG
670	680	690	700	710	720
*	*	*	*	*	*
GGTCTGCGGT	ATGGCGGGCA	AGGCGCGGTG	ATGCTGGAGC	CCGGCGTAGT	TATCGCCGCG
CCAGACGCCA	TACCGCCCGT	TCCGCGCCAC	TACGACCTCG	GGCCGCATCA	ATAGCGGGCG
730	740	750	760	770	780
*	*	*	*	*	*
ATGGCCTCGG	TGACCGAACA	TCTGGGGCTG	GGCGCCACCA	TTTCCACCAC	CTACTACCCG
TACCGGAGCC	ACTGGCTTGT	AGACCCCGAC	CCGCGGTGGT	AAAGGTGGTG	GATGATGGGC
790	800	810	820	830	840
*	*	*	*	*	*
CCCTACCATG	TAGCCCGGGT	CGTCGCTTCG	CTGGACCAGC	TGTCCTCCGG	GCGAGTGTCTG
GGGATGGTAC	ATCGGGCCCA	GCAGCGAAGC	GACCTGGTCTG	ACAGGAGGCC	CGCTCACAGC
850	860	870	880	890	900
*	*	*	*	*	*
TGGAACGTGG	TCACCTCGCT	CAGCAATGCA	GAGGCGCGCA	ACTTCGGCTT	CGATGAACAT
ACCTTGCAAC	AGTGGAGCGA	GTCGTTACGT	CTCCGCGCGT	TGAAGCCGAA	GCTACTTGTA
910	920	930	940	950	960
*	*	*	*	*	*
CTCGACCACG	ATGCCCCGTA	CGATCGCGCC	GATGAATTCC	TCGAGGTCGT	GCGCAAGCTC
GAGCTGGTGC	TACGGGCGAT	GCTAGCGCGG	CTACTTAAGG	AGCTCCAGCA	CGCGTTCGAG
970	980	990	1000	1010	1020
*	*	*	*	*	*
TGGAACAGCT	GGGATCGCGA	TGCGCTGACA	CTCGACAAGG	CAACCGGCCA	GTTCCGCCGAT
ACCTTGTCGA	CCCTAGCGCT	ACGCGACTGT	GAGCTGTTCC	GTTGGCCGGT	CAAGCGGCTA
1030	1040	1050	1060	1070	1080
*	*	*	*	*	*
CCGGCTAAGG	TGCGCTACAT	CGACCACCGC	GGCGAATGGC	TCAACGTACG	CGGGCCGCTT
GGCCGATTCC	ACGCGATGTA	GCTGGTGGCG	CCGCTTACCG	AGTTGCATGC	GCCCCGCGAA
1090	1100	1110	1120	1130	1140
*	*	*	*	*	*
CAGGTGCCGC	GCTCCCCCCA	GGGCGAGCCT	GTCATTCTGC	AGGCCGGGCT	TTCGGCGCGG
GTCCACGGCG	CGAGGGGGGT	CCCGCTCGGA	CAGTAAGACG	TCCGGCCCCA	AAGCCGCGCC
1150	1160	1170	1180	1190	1200
*	*	*	*	*	*
GGCAAGCGCT	TCGCCGGGCG	CTGGGCGGAC	GCGGTGTTCA	CGATTTTCGCC	CAATCTGGAC
CCGTTTCGCA	AGCGGCCCGC	GACCCGCCTG	CGCCACAAGT	GCTAAAGCGG	GTTAGACCTG

FIGURE 6B

1210	1220	1230	1240	1250	1260
*	*	*	*	*	*
ATCATGCAGG	CCACGTACCG	CGACATAAAG	GCGCAGGTCG	AGGCCGCCGG	ACGCGATCCC
TAGTACGTCC	GGTGCATGGC	GCTGTATTTT	CGCGTCCAGC	TCCGGCGGCC	TGCGCTAGGG
1270	1280	1290	1300	1310	1320
*	*	*	*	*	*
GAGCAGGTCA	AGGTGTTTGC	CGCGGTGATG	CCGATCCTCG	GCGAGACCGA	GGCGATCGCC
CTCGTCCAGT	TCCACAAACG	GCGCCACTAC	GGCTAGGAGC	CGCTCTGGCT	CCGCTAGCGG
1330	1340	1350	1360	1370	1380
*	*	*	*	*	*
AGGCAGCGTC	TCCAATACAT	AAATTCGCTG	GTGCATCCCG	AAGTCGGGGCT	TTCTACGTTG
TCCGTCGCAG	AGCTTATGTA	TTTAAGCGAC	CACGTAGGGC	TTCAGCCCCG	AAGATGCAAC
1390	1400	1410	1420	1430	1440
*	*	*	*	*	*
TCCAGCCATG	TCGGGGTCAA	CCTTGCCGAC	TATTCGCTCG	ATACCCCGCT	GACCGAGGTC
AGGTCGGTAC	AGCCCCAGTT	GGAACGGCTG	ATAAGCGAGC	TATGGGGCGA	CTGGCTCCAG
1450	1460	1470	1480	1490	1500
*	*	*	*	*	*
CTGGGCGATC	TCGCCCAGCG	CAACGTGCCC	ACCCAACCTGG	GCATGTTTCG	CAGGATGTTG
GACCCGCTAG	AGCGGGTCGC	GTTGCACGGG	TGGGTTGACC	CGTACAAGCG	GTCTTACAAC
1510	1520	1530	1540	1550	1560
*	*	*	*	*	*
CAGGCCGAGA	CGCTGACCGT	GGGAGAAATG	GGCCGGCGTT	ATGGCGCCAA	CGTGGGCTTC
GTCCGGCTCT	GCGACTGGCA	CCCTCTTTAC	CCGGCCGCAA	TACCGCGGTT	GCACCCGAAG
1570	1580	1590	1600	1610	1620
*	*	*	*	*	*
GTCCCGCAGT	GGGCGGGAAC	CCGCGAGCAG	ATCGCGGACC	TGATCGAGAT	CCATTTCAAG
CAGGGCGTCA	CCCGCCCTTG	GGCGCTCGTC	TAGCGCCTGG	ACTAGCTCTA	GGTAAAGTTT
1630	1640	1650	1660	1670	1680
*	*	*	*	*	*
GCCGGCGGCG	CCGATGGCTT	CATCATCTCG	CCGGCGTTCC	TGCCCCGATC	TTACGAGGAA
CGGCCGCCGC	GGCTACCGAA	GTAGTAGAGC	GGCCGCAAGG	ACGGGCCTAG	AATGCTCCTT
1690	1700	1710	1720	1730	1740
*	*	*	*	*	*
TTCTGTCGATC	AGGTGGTGCC	CATCCTGCAG	CACCGCGGAC	TGTTCGCGAC	TGATTACGAA
AAGCAGCTAG	TCCACCACGG	GTAGGACGTC	GTGGCGCCTG	ACAAGGCGTG	ACTAATGCCT
1750	1760	1770	1780	1790	1800
*	*	*	*	*	*
GGCCGCACCC	TGCGCAGCCA	TCTGGGACTG	CGTGAACCCG	CATACCTGGG	AGAGTACGCA
CCGGCGTGGG	ACGCGTCGGT	AGACCCTGAC	GCACTTGGGC	GTATGGACCC	TCTCATGCGT

FIGURE 6C

Sphingomonas dsz sequence (page 4)

1810 *	1820 *	1830 *	1840 *	1850 *	1860 *
TGACGACAGA	CATCCACCCG	GCGAGCGCCG	CATCGTCGCC	GGCGGCGCGC	GCGACGATCA
ACTGCTGTCT	GTAGGTGGGC	CGCTCGCGGC	GTAGCAGCGG	CCGCCGCGCG	CGCTGCTAGT
1870 *	1880 *	1890 *	1900 *	1910 *	1920 *
CCTACAGCAA	CTGCCCCGTG	CCTAATGCCC	TGCTCGCCGC	GCTCGGCTCA	GGTATTCTGG
GGATGTCGTT	GACGGGGCAC	GGATTACGGG	ACGAGCGGCG	CGAGCCGAGT	CCATAAGACC
1930 *	1940 *	1950 *	1960 *	1970 *	1980 *
ACAGTGCCGG	GATCACACTT	GCCCTGCTGA	CCGGAAGCA	GGGCGAGGTG	CACTTCACCT
TGTCACGGCC	CTAGTGTGAA	CGGGACGACT	GGCCTTTCGT	CCCGCTCCAC	GTGAAGTGA
1990 *	2000 *	2010 *	2020 *	2030 *	2040 *
ACGACCGAGA	TGACTACACC	CGCTTCGGCG	GCGAGATTCC	GCCGCTGGTC	AGCGAGGGAC
TGCTGGCTCT	ACTGATGTGG	GCGAAGCCGC	CGCTCTAAGG	CGGCGACCAG	TCGCTCCCTG
2050 *	2060 *	2070 *	2080 *	2090 *	2100 *
TGCGTGCGCC	GGGGCGGACC	CGCCTGCTGG	GACTGACGCC	GGTGCTGGGC	CGCTGGGGCT
ACGCACGCGG	CCCCGCCTGG	GCGGACGACC	CTGACTGCGG	CCACGACCCG	GCGACCCCGA
2110 *	2120 *	2130 *	2140 *	2150 *	2160 *
ACTTCGTCCG	GGGCGACAGC	GCGATCCGCA	CCCCGGCCGA	TCTTGCCGGC	CGCCGCGTCG
TGAAGCAGGC	CCCGCTGTCT	CGCTAGGCGT	GGGGCCGGCT	AGAACGGCCG	GCGGCGCAGC
2170 *	2180 *	2190 *	2200 *	2210 *	2220 *
GAGTATCCGA	TTCGGCCAGG	AGGATATTGA	CCGGAAGGCT	GGGCGACTAC	CGCGAACTTG
CTCATAGGCT	AAGCCGGTCC	TCCTATAACT	GGCCTTCCGA	CCCGCTGATG	GCGCTTGAAC
2230 *	2240 *	2250 *	2260 *	2270 *	2280 *
ATCCCTGGCG	GCAGACCCTG	GTCGCGCTGG	GGACATGGGA	GGCGCGTGCC	TTGCTGAGCA
TAGGGACCGC	CGTCTGGGAC	CAGCGCGACC	CCTGTACCCT	CCGCGCACGG	AACGACTCGT
2290 *	2300 *	2310 *	2320 *	2330 *	2340 *
CGCTCGAGAC	GGCGGGGCTT	GGCGTCGGCG	ACGTCGAGCT	GACGCGCATC	GAGAACCCGT
GCGAGCTCTG	CCGCCCCGAA	CCGCAGCCGC	TGCAGCTCGA	CTGCGCGTAG	CTCTTGGGCA
2350 *	2360 *	2370 *	2380 *	2390 *	2400 *
TCGTCGACGT	GCCGACCGAA	CGACTGCATG	CCGCCGGGCTC	GCTCAAAGGA	ACCGACCTGT
AGCAGCTGCA	CGGCTGGCTT	GCTGACGTAC	GGCGGCCGAG	CGAGTTTCCT	TGGCTGGACA

FIGURE 6D

Sphingomonas dsz sequence (page 5)

2410 *	2420 *	2430 *	2440 *	2450 *	2460 *
TCCCCGACGT	GACCAGCCAG	CAGGCCGCAG	TCCTTGAGGA	TGAGCGCGCC	GACGCCCTGT
AGGGGCTGCA	CTGGTCGGTC	GTCCGGCGTC	AGGAACTCCT	ACTCGCGCGG	CTGCGGGACA
2470 *	2480 *	2490 *	2500 *	2510 *	2520 *
TCGCGTGGCT	TCCCTGGGCG	GCCGAGCTCG	AGACCCGCAT	CGGTGCACGG	CCGGTCCTAG
AGCGCACCGA	AGGGACCCGC	CGGCTCGAGC	TCTGGGCGTA	GCCACGTGCC	GGCCAGGATC
2530 *	2540 *	2550 *	2560 *	2570 *	2580 *
ACCTCAGCGC	AGACGACCGC	AATGCCTATG	CGAGCACCTG	GACGGTGAGC	GCCGAGCTGG
TGGAGTCGCG	TCTGCTGGCG	TTACGGATAC	GCTCGTGGAC	CTGCCACTCG	CGGCTCGACC
2590 *	2600 *	2610 *	2620 *	2630 *	2640 *
TGGACCGGCA	GCCCGAACTG	GTGCAGCGGC	TCGTGATGTC	CGTGGTGGAT	GCAGGGCGGT
ACCTGGCCGT	CGGGCTTGAC	CACGTCGCCG	AGCAGCTACG	GCACCACCTA	CGTCCCGCCA
2650 *	2660 *	2670 *	2680 *	2690 *	2700 *
GGGCCGAGGC	CAATGGCGAT	GTGCTCTCCC	GCCTGCACGC	CGATAACCTC	GGTGTCAGTC
CCCGGCTCCG	GTTACCGCTA	CAGCAGAGGG	CGGACGTGCG	GCTATTGGAG	CCACAGTCAG
2710 *	2720 *	2730 *	2740 *	2750 *	2760 *
CCGAAAGCGT	CCGCCAGGGA	TTCGGAGCCG	ATTTTCACCG	CCGCCTGACG	CCGCGGCTCG
GGCTTTTCGCA	GGCGGTCCCT	AAGCCTCGGC	TAAAAGTGGC	GGCGGACTGC	GGCGCCGAGC
2770 *	2780 *	2790 *	2800 *	2810 *	2820 *
ACAGCGATGC	TATCGCCATC	CTGGAGCGTA	CTCAGCGGTT	CCTGAAGGAT	GCGAACCTGA
TGTCGCTACG	ATAGCGGTAG	GACCTCGCAT	GAGTCGCCAA	GGACTTCCTA	CGCTTGGAAT
2830 *	2840 *	2850 *	2860 *	2870 *	2880 *
TCGATCGGTC	GTTGGCGCTC	GATCGGTGGG	CTGCACCTGA	ATTCCTCGAA	CAAAGTCTCT
AGCTAGCCAG	CAACCGCGAG	CTAGCCACCC	GACGTGGACT	TAAGGAGCTT	GTTTCAGAGA
2890 *	2900 *	2910 *	2920 *	2930 *	2940 *
CACGCCAGGT	CGAAGGGCAG	ATAGCATGAA	CGAACTCGTC	AAAGATCTCG	GCCTCAATCG
GTGCGGTCCA	GCTTCCCGTC	TATCGTACTT	GCTTGAGCAG	TTTCTAGAGC	CGGAGTTAGC
2950 *	2960 *	2970 *	2980 *	2990 *	3000 *
ATCCGATCCG	ATCGGCGCTG	TGCGGCGACT	GGCCGCGCAG	TGGGGGGCCA	CCGCTGTTGA
TAGGCTAGGC	TAGCCGCGAC	ACGCGCTGA	CCGGCGCGTC	ACCCCCCGGT	GGCGACAACCT

FIGURE 6E

Sphingomonas dsz sequence (page 6)

3010	3020	3030	3040	3050	3060
*	*	*	*	*	*
TCGGGACCGG	GCCGGCGGAT	CGGCAACCGC	CGAACTCGAT	CAACTGCGCG	GCAGCGGCCCT
AGCCCTGGCC	CGGCCGCCTA	GCCGTTGGCG	GCTTGAGCTA	GTTGACGCGC	CGTCGCCCGA
3070	3080	3090	3100	3110	3120
*	*	*	*	*	*
GCTCTCGCTG	TCCATTCCCG	CCGCATATGG	CGGCTGGGGC	GCCGACTGGC	CAACGACTCT
CGAGAGCGAC	AGGTAAGGGC	GGCGTATACC	GCCGACCCCG	CGGCTGACCG	GTTGCTGAGA
3130	3140	3150	3160	3170	3180
*	*	*	*	*	*
GGAAGTTATC	CGCGAAGTCG	CAACGGTGGA	CGGATCGCTG	GCGCATCTAT	TCGGCTACCA
CCTTCAATAG	GCGCTTCAGC	GTTGCCACCT	GCCTAGCGAC	CGCGTAGATA	AGCCGATGGT
3190	3200	3210	3220	3230	3240
*	*	*	*	*	*
CCTCGGCTGC	GTACCGATGA	TCGAGCTGTT	CGGCTCGGGC	CCACAAAAGG	AACGGCTGTA
GGAGCCGACG	CATGGCTACT	AGCTCGACAA	GCCGAGCCGC	GGTGTTTTCC	TTGCCGACAT
3250	3260	3270	3280	3290	3300
*	*	*	*	*	*
CCGCCAGATC	GCAAGCCATG	ATTGGCGGGT	CGGGAATGCG	TCGAGCGAAA	ACAACAGCCA
GGCGGTCTAG	CGTTCGGTAC	TAACCGCCCA	GCCCTTACGC	AGCTCGCTTT	TGTTGTCTGGT
3310	3320	3330	3340	3350	3360
*	*	*	*	*	*
CGTGCTCGAG	TGGAAGCTTG	CCGCCACCGC	CGTCGATGAT	GGCGGGTTTC	TCCTCAACGG
GCACGAGCTC	ACCTTCGAAC	GGCGGTGGCG	GCAGCTACTA	CCGCCCCAAGC	AGGAGTTGCC
3370	3380	3390	3400	3410	3420
*	*	*	*	*	*
CGCGAAGCAC	TTCTGCAGCG	GCGCCAAAAG	CTCCGACCTG	CTCATCGTGT	TCGGCGTGAT
GCGCTTCGTG	AAGACGTCGC	CGCGGTTTTT	GAGGCTGGAC	GAGTAGCACA	AGCCGCACTA
3430	3440	3450	3460	3470	3480
*	*	*	*	*	*
CCAGGACGAA	TCCCCCTGC	GCGGCGCGAT	CATCACCGCG	GTCATTCCCA	CCGACCGGGC
GGTCCTGCTT	AGGGGGGACG	CGCCGCGCTA	GTAGTGGCGC	CAGTAAGGGT	GGCTGGCCCG
3490	3500	3510	3520	3530	3540
*	*	*	*	*	*
CGGTGTTTAC	ATCAATGACG	ACTGGCGCGC	AATCGGGATG	CGCCAGACCG	ACAGCGGCAG
GCCACAAGTC	TAGTTACTGC	TGACCGCGCG	TTAGCCCTAC	GCGGTCTGGC	TGTCGCCGTC
3550	3560	3570	3580	3590	3600
*	*	*	*	*	*
CGCCGAATTT	CGCGACGTCC	GAGTCTACCC	AGACGAGATC	TTGGGGGCAC	CAAACCTCAGT
GCGGCTTAAA	GCGCTGCAGG	CTCAGATGGG	TCTGCTCTAG	AACCCCGTGT	GTTTGAGTCA

FIGURE 6F

Sphingomonas dsz sequence (page 7)

3610 *	3620 *	3630 *	3640 *	3650 *	3660 *
CGTTGAGGCG	TTCGTGACAA	GCAACCGCGG	CAGCCTGTGG	ACGCCGGCGA	TTCAGTCGAT
GCAACTCCGC	AAGCACTGTT	CGTTGGCGCC	GTCGGACACC	TGCGGCCGCT	AAGTCAGCTA
3670 *	3680 *	3690 *	3700 *	3710 *	3720 *
CTTCTCGAAC	GTTTATCTGG	GGCTCGCGCG	TGGCGCGCTC	GAGGCGGCAG	CGGATTACAC
GAAGAGCTTG	CAAATAGACC	CCGAGCGCGC	ACCGCGCGAG	CTCCGCCGTC	GCCTAATGTG
3730 *	3740 *	3750 *	3760 *	3770 *	3780 *
CCGGACCCAG	AGCCGCCCT	GGACACCCGC	CGGCGTGGCG	AAGGCGACAG	AGGATCCCCA
GGCTGGGTC	TCGGCGGGA	CCTGTGGGCG	GCCGCACCGC	TTCCGCTGTC	TCCTAGGGGT
3790 *	3800 *	3810 *	3820 *	3830 *	3840 *
CATCATCGCC	ACCTACGGTG	AACTGGCGAT	CGCGCTCCAG	GGCGCCGAGG	CGGCCGCGCG
GTAGTAGCGG	TGGATGCCAC	TTGACCGCTA	GCGCGAGGTC	CCGCGGCTCC	GCCGGCGCGC
3850 *	3860 *	3870 *	3880 *	3890 *	3900 *
CGAGGTGCGG	GCCCTGTTGC	AACAGGCGTG	GGACAAGGGC	GATGCGGTGA	CGCCCGAAGA
GCTCCAGCGC	CGGGACAACG	TTGTCCGCAC	CCTGTTCCCG	CTACGCCACT	GCGGGCTTCT
3910 *	3920 *	3930 *	3940 *	3950 *	3960 *
GCGCGGCCAG	CTGATGGTGA	AGGTTTCGGG	TGTGAAGGCC	CTCTCGACGA	AGGCCGCCCT
CGCGCCGGTC	GACTACCACT	TCCAAAGCCC	ACACTTCCGG	GAGAGCTGCT	TCCGGCGGGA
3970 *	3980 *	3990 *	4000 *	4010 *	4020 *
CGACATCACC	AGCCGTATTT	TCGAGACAAC	GGGCTCGCGA	TCGACGCATC	CCAGATACGG
GCTGTAGTGG	TCGGCATAAA	AGCTCTGTTG	CCCAGCGCT	AGCTGCGTAG	GGTCTATGCC
4030 *	4040 *	4050 *	4060 *	4070 *	4080 *
ATTCGATCGG	TTCTGGCGTA	ACATCCGGAC	TCATACGCTG	CACGATCCGG	TATCGTATAA
TAAGCTAGCC	AAGACCGCAT	TGTAGGCCTG	AGTATGCGAC	GTGCTAGGCC	ATAGCATATT
4090 *	4100 *	4110 *	4120 *	4130 *	4140 *
AATCGTCGAT	GTGGGGAAC	ACACGCTCAA	CGGGACATTC	CCGGTTCCCG	GATTTACGTC
TTAGCAGCTA	CACCCCTTGA	TGTGCGAGTT	GCCCTGTAAG	GGCCAAGGGC	CTAAATGCAG
ATGA					
TACT					

FIGURE 6G

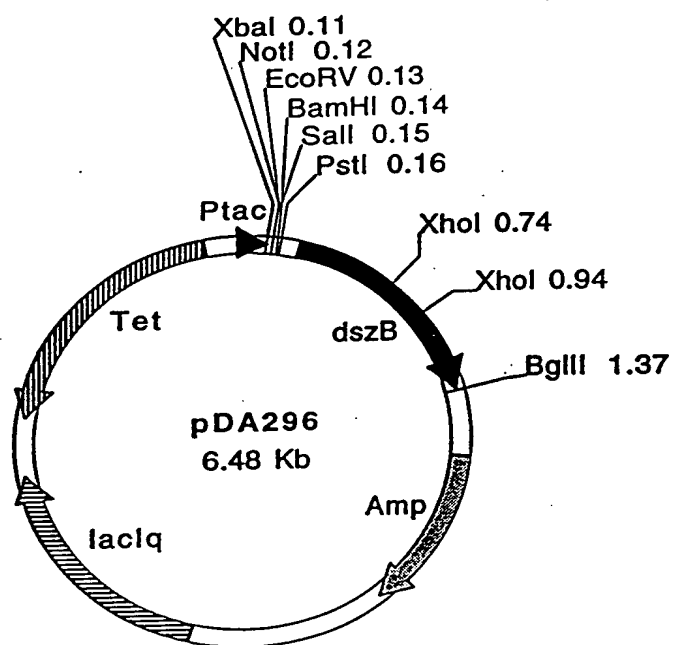


FIGURE 7

DsZa (S)	1	MTDPRQLHLAGFFCAGNVTHAHGAWRHADDSNGFLTKEYYQQIARTLERG	50
		. : : : . : . . :	
DsZa (R)	1	MTQQRQMHLAGFFSAGNVTHAHGAWRHTDASNDFLSGKYYQHIARTLERG	50
DsZa (S)	51	KFDLLFLPDALAVWDSYGDNLETGLRYGGQGAVMLEPGVVIAAMASVTEH	100
		: : : . : : . .	
DsZa (R)	51	KFDLLFLPDGLAVEDSYGDNLDTGVLGGQGAVALEPASVVATMAAVTEH	100
DsZa (S)	101	LGLGATISTTYYPPYHVARVVASLDQLSSGRVSWNVVTSLSNAEARNFGF	150
		. . . : . : :	
DsZa (R)	101	LGLGATISATYYPPYHVARVFATLDQLSGGRVSWNVVTSLNDAEARNFGI	150
DsZa (S)	151	DEHLDHDARYDRADEFLEVVRKLNWSWDRDALTLDKATGQFADPAKVRYI	200
		:: : . : . . : :	
DsZa (R)	151	NQHLEHDARYDRADEFLEAVKKLNWSWDEDALVLDKAAGVFADPAKVHYV	200
DsZa (S)	201	DHRGEWLNVRGPLQVPRSPQGEFVILQAGLSARGKRFAGRWADAVFTISP	250
		: . . : : : : : : : : : : : :	
DsZa (R)	201	DHHGEWLNVRGPLQVPRSPQGEFVILQAGLSRGRRFAGKWAEAVFSLAP	250
DsZa (S)	251	NLDIMQATYRDIKAQVEAAGRDPEQVKVFAAVMPILGETEAIARQRLLEYI	300
		:: . : : : : : : : . : . : : : : : : :	
DsZa (R)	251	NLEVMQATYQGIKAEVDAAGRDPDQTKIFTAVMPVLGESQAVAQERLEYL	300
DsZa (S)	301	NSLVHPEVGLSTLSSHVGVNLDYSLDTPLTEVLGDLAQRNVPTQLGMFA	350
		. : : . : : : : : : :	
DsZa (R)	301	NSLVHPEVGLSTLSSHTGINLAAYPLDTPIKDILRDLQDRNVPTQLHMF	350
DsZa (S)	351	RMLQAETLTVGEMGRRYGANVGFPQWAGTREQIADLIEIHFKAGGADGF	400
		: . : : : : : : : : : : :	
DsZa (R)	351	AATHSEELTLAEMGRRYGTNVGFPQWAGTGEQIADLIRHFEGGAADGF	400
DsZa (S)	401	IISPAFLPGSYEEFVDQVVPILQHRGLFRDYEGRTLRSHLGLREPAYLG	450
		: : : . . : :	
DsZa (R)	401	IISPAFLPGSYDEFVDQVVPVLQDRGYFRTEYQGNLRLDHLGLRVPQLQG	450
DsZa (S)	451	EYA 453	
		:	
DsZa (R)	451	QPS 453	

FIGURE 8

DszB (S)	MTTDIHPASAASSPAA--RATITYSNCPVPNALLAALGSGILDSAGITLALL	50
DszB	MTSRVDPANPGSELDSAIRD TL TYSNCPVPNALLTASESGFLDAAGIELDVL	52
DszB (S)	TGKQGEVHFTYDRDDYTRFGGEIPPLVSEGLRAPGRTRLLGLTPVLGRWGYF	102
DszB	SGQQGT VH FTYDQPAYTRFGGEIPPLLSEGLRAPGRTRLLGITPLLGRQGFF	104
DszB (S)	VRGDSAIRTPADLAGRRVGVSDSARRILTGRIGDYRELD PWRQ TLVALGTWE	154
DszB	VRDDSPITAAADLAGRRIGVSASAIRILRGQLGDYLELD PWRQ TLVALGSWE	156
DszB (S)	ARALLSTLETAGLGVGDVELTR EN PFVDVPTERLHAAGSLKGTDLFPD VTS	206
DszB	ARALLHTLEHGELGVDDVELVPISSPGVDVPAEQLEESATVKGADLFPDVAR	208
DszB (S)	QAAVLEDERADALFAWL PWAA ELETRIGARPVLDLSADDRNAYASTWTVSA	258
DszB	GQAAVLASGDVDALYSWL PWAGELQA -TGARPVVDLGLDERNAYASVWTVSS	260
DszB (S)	ELVDRQPELVQRLVDAVVDAGR WAE ANGDVVSRLHADNLGVSPESVRQGF GA	310
DszB	GLVRQRPGLVQRLVDAVVDAGLWARDHSDAVTSLHAANLGVSTGAVGQGF GA	312
DszB (S)	DFHRRLT PR LDSDAIAILERTQ R FLKDANLIDRSLALDRWAAPEFLEQSLSRQVEGQIA	369
DszB	DFQ Q RLVPRLDH D ALALLERTQ Q FLLTNNLLQEPVALDQWAAPEFLNNSLN R HR	365

FIGURE 9

DszC(S) 1MNELVKDLGLNRS DPIGAVRRLAAQWGATAVDRDRAGGSATAELD 45
 DszC(R) 1 MTLSPKQHVPRDAADNDPVA VARGLA EKWRATAVERDRAGGSATAERE 50
 DszC(S) 46 QLRGSGLLSL SIPAAYGGWGADWPTTLEVIREVATVDGSLAHLFGYHLGC 95
 DszC(R) 51 DLRASALLSLLVPREYGGWGADWPTAIEVVREIAAADGSLGHLFGYHLTN 100
 DszC(S) 96 VPMIELFGSAPQKERLYRQIASHDWRVGNASSENNSHVLEWKLAATAVDD 145
 DszC(R) 101 APMIELIGSQEQEEHLYTQIAQNNWWTGNASSENNSHVLDWKVSATPTED 150
 DszC(S) 146 GGFVLNGAKHFCSGAKSSDLLIVFGVQDESPLRGAIITAVIPTDRAGVQ 195
 DszC(R) 151 GGYVLNGTKHFCSGAKGSDLLFVFGVVQDDSPQQGAIIAAAIPTSRAGVT 200
 DszC(S) 196 INDDWRAIGMRQTDSGSAEFRDVRVYPDEILGAPNSVVEAFVTSNRGSLW 245
 DszC(R) 201 PNDDWAAIGMRQTDSGSTDFHNVKVEPDEV LGAPNAFVLAFIQSERGSLF 250
 DszC(S) 246 TPAIQSIFSNVYLGLARGALEAAADYTRTQSRPWTPAGVAKATEDPHIIA 295
 DszC(R) 251 APIAQLIFANVYLGIAHGALDAAREYTRTQARPWTPAGIQQATEDPYTIR 300
 DszC(S) 296 TYGELAIALQGAEEAAAREVAALLQQAWDKGDVTPPEERGQLMKVSGVKA 345
 DszC(R) 301 SYGEFTIALQGADAAAREAAHLLQTVWDKGDALTPEDRGELMKVSGVKA 350
 DszC(S) 346 LSTKAALDITSRIFETTGSRSTHPRYGFDRFWRNIRTHTLHDPVSYKIVD 395
 DszC(R) 351 LATNAALNISSGVFEVIGARGTHPRYGFDRFWRNVRTSLHDPVSYKIAD 400
 DszC(S) 396 VGNYTLNGTFPVPGFST 412
 DszC(R) 401 VGKHTLNGQYPIPGFTS 417

FIGURE 10

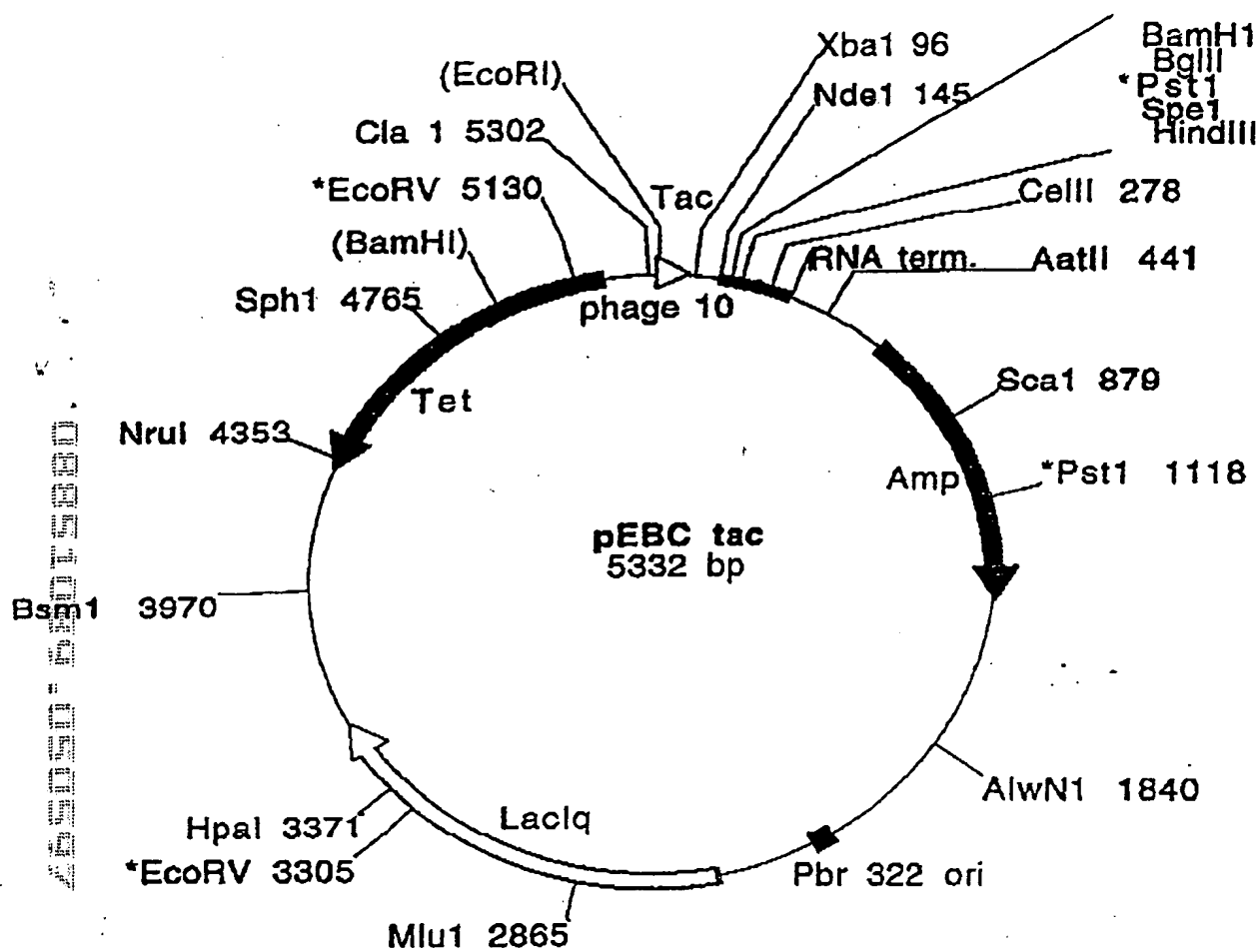


FIGURE 11